Freeform Search

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Search History			

DATE: Monday, October 13, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB = US	SPT; PLUR = YES; OP = OR		
<u>L7</u>	16 and 13	2	<u>L7</u>
<u>L6</u>	encoding DNA and 11	120990	<u>L6</u>
<u>L5</u>	13 and L4	0	<u>L5</u>
<u>L4</u>	jones.in.	11873	<u>L4</u>
<u>L3</u>	l1 and L2	83	<u>L3</u>
<u>L2</u>	stubbs.in.	252	<u>L2</u>
<u>L1</u>	modified green fluorescent protein	903177	<u>L1</u>

END OF SEARCH HISTORY

End of Result Set

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L10: Entry 1 of 1 File: USPT Jul 7, 1998

DOCUMENT-IDENTIFIER: US 5777079 A

** See image for Certificate of Correction **
TITLE: Modified green fluorescent proteins

TITLE: Modified green fluorescent proteins

<u>US Patent No.</u> (1): 5777079

Detailed Description Text (5):

A molecular interpretation is presented in FIG. 2. If the newly translated apoprotein (top left) evades precipitation into inclusion bodies, the amino group of Gly 67 might cyclize onto the carbonyl group of Ser 65 to form an imidazolidin-5-one, where the process would stop (top center) if O.sub.2 is absent. The new N=C double bond would be expected to promote dehydrogenation to form a conjugated chromophore; imidazolidin-5-ones are indeed known to undergo autoxidative formation of double bonds at the 4-position [Kjaer, A. Acta Chem. Scand. 7, 1030-1035 (1953); Kidwai, A. R. & Devasia, G. M. J. Org. Chem. 27, 4527-4531 (1962)], which is exactly what is necessary to complete the fluorophore (upper right). The protonated and deprotonated species (upper and lower right) may be responsible for the 395 and 470-475 nm excitation peaks, respectively. The excited states of phenols are much more acidic than their ground states, so that emission would come only from a deprotonated species.

Detailed Description Text (7):

According to a first aspect of the present invention, modifications are provided which result in a shift in the ratio of the two excitations peaks of the product after oxidation and cyclization relative to the wild type. Three mutants were found with significant alterations in the ratio of the two main excitation peaks (Table I). The mutations were sequenced and recombined with the wild-type gene in different ways to eliminate neutral mutations and assign the fluorescence effects to single amino acid substitutions, except for H9 where two neighboring mutations have not yet been separated. They all lay in the C terminal part of the protein (Table I), remote in primary sequence from the chromophore formed from residues 65-67.

Detailed Description Text (8):

These and other modifications are defined herein with reference to the amino acid sequence [SEQ ID NO:2] encoded by the reported cDNA [SEQ ID NO:1]; the first amino acid identified is the one found at the indicated location in the reported sequence, while the second indicates the substitution found in the modified form. The fluorescent product derived from a wild-type or modified GFP polypeptide sequence is no longer strictly speaking a simple polypeptide after oxidation and cyclization; however, reference is sometimes made for sake of simplicity herein to the polypeptide (e.g., "wild-type GFP" or "modified GFP") where what is intended would be obvious from the context. Compared with wild-type GFP, H9 (Ser 202.fwdarw.Phe, Thr 203.fwdarw.Ile) had increased fluorescence at 395 nm excitation; P9 (Ile 167.fwdarw.Val) and P11 (Ile 167.fwdarw.Thr) were more fluorescent at 475 nm excitation.

Detailed Description Text (10):

According to another aspect of the invention, a mutant P4 (Tyr 66.fwdarw.His) was identified which was excitable by ultraviolet and fluoresced bright blue in contrast to the green of wild type protein. The excitation and emission maxima were

hypsochromically shifted by 14 and 60 nm respectively from those of wild-type GFP. The mutated DNA was sequenced and found to contain five amino acid substitutions, only one of which proved to be critical: replacement of Tyr 66 in the center of the chromophore by His (corresponding to a change in the GFP cDNA sequence [SEQ ID NO:1] at 196-198 from TAT to CAT).

Detailed Description Text (11):

The surprising tolerance for substitution at this key residue prompted further site-directed mutagenesis to Trp and Phe at this position. Trp gave excitation and emission wavelengths intermediate between Tyr and His (Table I) but was only weakly fluorescent, perhaps due to inefficiency of folding or chromophore formation due to steric considerations. Phe gave weak fluorescence with an excitation maximum at 358 nm and an emission maximum at 442 nm. Accordingly, pursuant to this aspect of the invention modified GFP proteins which fluoresce at different wavelengths (preferably, different by at least 10 nm and more preferably, by at least 50 nm) relative to the native protein are provided, for example, those wherein Tyr 66 is replaced by Phe, His or Trp.

Detailed Description Text (13):

In accordance with further embodiments of this aspect of the invention, a first round of mutagenesis to increase the brightness of Y66W yielded M153T/V163A/N212K as additional substitutions. This mutant was subjected to another round of mutagenesis, resulting in two further sets, N146I and I123V/Y145H/H148R (Table II). The quantum efficiency of these mutants is now comparable to wild-type GFP. The clustering of the substitutions in residues 145 to 163 suggest that those residues lie relatively close to the chromophore and that reductions in the size of their side chains might be compensating for the larger size of tryptophan compared to tyrosine.

Detailed Description Text (15):

Mutagenesis of S65T to shift its wavelengths further to the red yielded M153A/K238E (Table II) as the GFP variant with the longest-wavelength excitation maximum yet described, 504 nm vs. 490 nm for S65T. Surprisingly, the emission peak hardly changed (514 nm vs. 511 nm), so that the separation between the excitation and emission peaks (Stokes' shift) is extremely narrow, only 10 nm. This is one of the smallest values reported for any fluorophore in aqueous solution at room temperature. As in the Y66W series, M153 seems to be influential. It is doubtful that K238E is important, because this substitution has been found to be without effect in other mutants.

Detailed Description Text (16):

As would be readily apparent to those working in the field, to provide the desired fluorescent protein it would not be necessary to include the entire sequence of GFP. In particular, minor deletions at either end of the protein sequence are expected to have little or no impact on the fluorescence spectrum of the protein. Therefore, by a mutant or wild-type GFP sequence for purposes of the present invention are contemplated not only the complete polypeptide and oligonucleotide sequences discussed herein, but also functionally-equivalent portions thereof (i.e., portions of the polypeptide sequences which exhibit the desired fluorescence properties and oligonucleotide sequences encoding these polypeptide sequences). For example, whereas the chromophore itself (position 65-67) is obviously crucial, the locations of known neutral mutations suggest that amino acids 76-115 are less critical to the spectroscopic properties of the product. In addition, as would be immediately apparent to those working in the field, the use of various types of fusion sequences which lengthen the resultant protein and serve some functional purpose in the preparation or purification of the protein would also be routine and are contemplated as within the scope of the present invention. For example, it is common practice to add amino acid sequences including a polyhistidine tag to facilitate purification of the product proteins. As such fusions do not significantly alter the salient properties of the molecules comprising same, modified GFPs as described herein including such fusion sequences at either end thereof are also clearly contemplated as within the scope of the present invention.

Detailed Description Text (17): Similarly, in addition to the specific mutations disclosed herein, it is well understood by those working in the field that in many instances modifications in

particular locations in the polypeptide sequence may have no effect upon the properties of the resultant polypeptide. Unlike the specific mutations described in detail herein, other mutations provide polypeptides which have properties essentially or substantially indistinguishable from those of the specific polypeptides disclosed herein. For example, the following substitutions have been found to be neutral (i.e., have no significant impact on the properties of the product): Lys 3.fwdarw.Arg; Asp 76.fwdarw.Gly; Phe 99.fwdarw.Ile; Asn 105.fwdarw.Ser; Glu 115.fwdarw.Val; Thr 225.fwdarw.Ser; and Lys 238.fwdarw.Glu. These equivalent polypeptides (and oligonucleotide sequences encoding these polypeptides) are also regarded as within the scope of the present invention. In general, the polypeptides and oligonucleotide sequences of the present invention (in addition to containing at least one of the specific mutations identified herein) will be at least about 85 % homologous, more preferably at least about 90% homologous, and most preferably at least about 95% homologous, to the wild-type GFP described herein. Because of the significant difference in properties observed upon introduction of the specified modifications into a GFP sequence, the presence of the specified modifications relative to the corresponding reported sequence for wild-type GFP [SEQ ID NO:2] are regarded as central to the invention.

Detailed Description Text (22):

The chromophore in GFP is well buried inside the rest of the protein, so much of the dimness of the original point mutants was presumably due to steric mismatch between the substituted amino acid and the cavity optimized for tyrosine. The location of the beneficial mutations implies that residues 145-163 are probably close to the chromophore. The M153A/S65T mutant has the longest wavelengths and smallest Stokes'shift of any known fluorescent protein that does not use a cofactor.

Detailed Description Text (30):

Oligonucleotide-directed mutagenesis at the codon for Ser-65 of GFP cDNA was performed by the literature method [Kunkel, T. A. (1985) Proc. Natl. Acad. Sci. USA 82, 488] using the Muta-Gene Phagemid in Vitro Mutagenesis Kit version 2, commercially available from Bio-Rad, Richmond, Calif. The method employs a bacterial host strain deficient for dUTPase (dut) and uracil-N-glycosylase (ung), which results in an occasional substitution of uracil for thymine in newly-synthesized DNA. When the uracil-containing DNA is used as a wild-type template for oligonucleotide-directed in vitro mutagenesis, the complementary (mutant) strand can be synthesized in the presence of deoxynucleotides, ligase and polymerase using the mutagenic oligonucleotide to prime DNA synthesis; the Version 2 kit utilizes unmodified T7 DNA polymerase to synthesize the complementary strand. When the heteroduplex molecule is transformed into a host with an active uracil-N-glycosylase (which cleaves the bond between the uracil base and the ribose molecule, yielding an apyrimidic site), the uracil-containing wild-type strand is inactivated, resulting in an enrichment of the mutant strand.

Detailed Description Text (42):

Excitation spectra were obtained by collecting emission at the respective peak wavelengths and were corrected by a Rhodamine B quantum counter. Emission spectra were likewise measured at the respective excitation peaks and were corrected using factors from the fluorometer manufacturer (Spex Industries, Edison, N.J.). In cleavage experiments emission spectra were recorded at excitation 368 nm. For measuring molar extinction coefficients, 20 to 30 .mu.g of protein were used in 1 ml of PBS pH 7.4. Quantum yields of wild-type GFP, S65T, and P4-1 mutants were estimated by comparison with fluorescein in 0.1 N NaOH as a standard of quantum yield 0.91 [ed. Miller, J. N., Standards in Fluorescence Spectrometry (Chapman and Hall, New York, 1981)]. Mutants P4 and P4-3 were likewise compared to 9-amino-acridine in water (quantum yield 0.98). W2 and W7 were compared to both standards, which fortunately gave concordant results.

Detailed Description Paragraph Table (3):

SEQUENCE

LISTING (1) GENERAL INFORMATION: (iii) NUMBER OF SEQUENCES: 2 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 716 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..716 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: ATGAGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAATTCTTGTT48

MetSerLysGlyGluGluLeuPheThrGlyValValProIleLeuVal 151015 GAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCAGTGGAGAG96 GluLeuAspGlyAspValAsnGlyHisLysPheSerValSerGlyGlu 202530 GlyGluGlyAspAlaThrTyrGlyLysLeuThrLeuLysPheIleCys 354045 ACTACTGGAAAACTACCTGTTCCATGGCCAACACTTGTCACTACTTTC192 ThrThrGlyLysLeuProValProTrpProThrLeuValThrThrPhe 505560 TCTTATGGTGTTCAATGCTTTTCAAGATACCCAGATCATATGAAACAG240 SerTyrGlyValGlnCysPheSerArgTyrProAspHisMetLysGln 65707580 CATGACTTTTTCAAGAGTGCCATGCCCGAAGGTTATGTACAGGAAAGA288 HisAspPhePheLysSerAlaMetProGluGlyTyrValGlnGluArg 859095 ACTATATTTTCAAAGATGACGGGAACTACAAGACACGTGCTGAAGTC336 ThrIlePhePheLysAspAspGlyAsnTyrLysThrArgAlaGluVal 100105110 AAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTTAAAAGGTATT384 LysPheGluGlyAspThrLeuValAsnArgIleGluLeuLysGlyIle 115120125 GATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACAAC432 AspPheLysGluAspGlyAsnIleLeuGlyHisLysLeuGluTyrAsn 130135140 TyrAsnSerHisAsnValTyrIleMetAlaAspLysGlnLysAsnGly 145150155160 ATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTT528 IleLysValAsnPheLysIleArgHisAsnIleGluAspGlySerVal 165170175 CAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCT576 GlnLeuAlaAspHisTyrGlnGlnAsnThrProIleGlyAspGlyPro 180185190 GTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCG624 ValLeuLeuProAspAsnHisTyrLeuSerThrGlnSerAlaLeuSer 195200205 AAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTA672 LysAspProAsnGluLysArgAspHisMetValLeuLeuGluPheVal 210215220 ACAGCTGCTGGGATTACACATGGCATGGATGAACTATACAAATA716 ThralaAlaGlyIleThrHisGlyMetAspGluLeuTyrLys 225230235 (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: MetSerLysGlyGluGluLeuPheThrGlyValValProIleLeuVal 151015 GluLeuAspGlyAspValAsnGlyHisLysPheSerValSerGlyGlu 202530 GlyGluGlyAspAlaThrTyrGlyLysLeuThrLeuLysPheIleCys 354045 ThrThrGlyLysLeuProValProTrpProThrLeuValThrThrPhe 505560 SerTyrGlyValGlnCysPheSerArgTyrProAspHisMetLysGln 65707580 HisAspPhePheLysSerAlaMetProGluGlyTyrValGlnGluArg 859095 ThrIlePhePheLysAspAspGlyAsnTyrLysThrArgAlaGluVal 100105110 LysPheGluGlyAspThrLeuValAsnArgIleGluLeuLysGlyIle 115120125 AspPheLysGluAspGlyAsnIleLeuGlyHisLysLeuGluTyrAsn 130135140 TyrAsnSerHisAsnValTyrIleMetAlaAspLysGlnLysAsnGly 145150155160 IleLysValAsnPheLysIleArgHisAsnIleGluAspGlySerVal 165170175 GlnLeuAlaAspHisTyrGlnGlnAsnThrProIleGlyAspGlyPro 180185190 ValLeuLeuProAspAsnHisTyrLeuSerThrGlnSerAlaLeuSer 195200205 LysAspProAsnGluLysArgAspHisMetValLeuLeuGluPheVal 210215220 ThrAlaAlaGlyIleThrHisGlyMetAspGluLeuTyrLys 225230235

CLAIMS:

- 1. A composition of matters comprising:
- a fluorescent modified form of an Aequorea wild-type GPP polypeptide,

characterized in that upon oxidation and cyclization of amino-acid residues in said fluorescent modified form corresponding to positions 65 to 67 of wild-type GFP polypeptide sequence (SEQ ID NO:2) said fluorescent modified form exhibits a different excitation and/or emission spectrum from a corresponding product of said wild-type GFP polypeptide sequence,

with the proviso that when said fluorescent modified form comprises a mutation at S65, said mutation at S65 is selected from the group consisting of S65A, S65C, S65T, S65L, S65V, and S65I.

14. The composition according to claim 13,

wherein said fluorescent modified comprises a replacement of Ser at a position corresponding to position 65 of said wild-type GFP polypeptide sequence by an amino acid selected from the group consisting of Ala, Cys, Thr, Leu, Val and Ile.

15. The composition according to claim 14,

wherein said amino acid is Cys of Thr.

16. A functional mutant fluorescent protein, comprising:

a protein with an <u>amino acid</u> sequence that differs from an <u>amino acid</u> sequence of an Aequorea wild type green fluorescent protein (SEQ ID NO:2) by at least one <u>amino acid substitution</u> that is at position 65, wherein said at least one <u>substitution</u> is either S65A, S65C, S65T, S65L, S65V, or S651,

- wherein said functional mutant fluorescent protein has an excitation or emission different from an excitation spectrum or emission spectrum of said Aequorea wild type green fluorescent protein.
 - 17. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65A.

19. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65C.

21. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65T.

23. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65L.

25. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65V.

27. The functional mutant fluorescent protein of claim 16,

wherein said at least one amino acid substitution that is at position 65 is S65I.

31. The functional mutant fluorescent protein of claim 16,

wherein said functional mutant fluorescent protein further comprises an amino acid sequence which targets said protein to the specific cellular locations.

32. A functional mutant fluorescent protein, comprising:

a protein with an amino acid sequence that differs from an amino acid sequence of an Aequorea wild type green fluorescent protein (SEQ ID NO:2) by at least one amino acid substitution that is at position 66, wherein said at least one substitution is either Y66H or Y66W, further wherein said functional mutant fluorescent protein has an excitation or emission different from an excitation spectrum or emission spectrum of said Aequorea wild type green fluorescent protein.

33. The functional mutant fluorescent protein of claim 32,

wherein said at least one amino acid substitution that is at position 66 is Y66W.

35. The functional mutant fluorescent protein of claim 32,

wherein said at least one amino acid substitution that is at position 66 is Y66H.

43. A functional mutant fluorescent protein, comprising:

a protein with an <u>amino acid</u> sequence that differs from an <u>amino acid</u> sequence of an Aequorea wild type green fluorescent protein (SEQ ID NO:2) by at least one <u>amino</u> acid substitution in the region consisting of positions 65 and 66,

wherein said functional mutant fluorescent protein has an excitation or emission different from an excitation spectrum or emission spectrum of said Aequorea wild type green fluorescent protein.

46. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 202.

47. The functional mutant fluorescent protein of claim 46,

wherein said amino acid substitution that is at position 202 is S202F.

48. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 203.

49. The functional mutant fluorescent protein of claim 48,

wherein said amino acid substitution that is at position 203 is T203I.

50. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 167.

51. The functional mutant fluorescent protein of claim 50,

wherein said amino acid substitution that is at position 167 is I167 V or I167T.

52. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 153.

53. The functional mutant fluorescent protein of claim 52,

wherein said amino acid substitution that is at position 153 is M153T or M153A.

54. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 238.

55. The functional mutant fluorescent protein of claim 54,

wherein said amino acid substitution that is at position 238 is K238E.

56. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 145.

57. The functional mutant fluorescent protein of claim 56,

wherein said amino acid substitution that is at position 145 is Y145H or Y145F.

58. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 146.

59. The functional mutant fluorescent protein of claim 58,

wherein said amino acid substitution that is at position 146 is N146I.

60. The functional mutant fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 163 or 148.

61. The functional mutant fluorescent protein of claim 60,

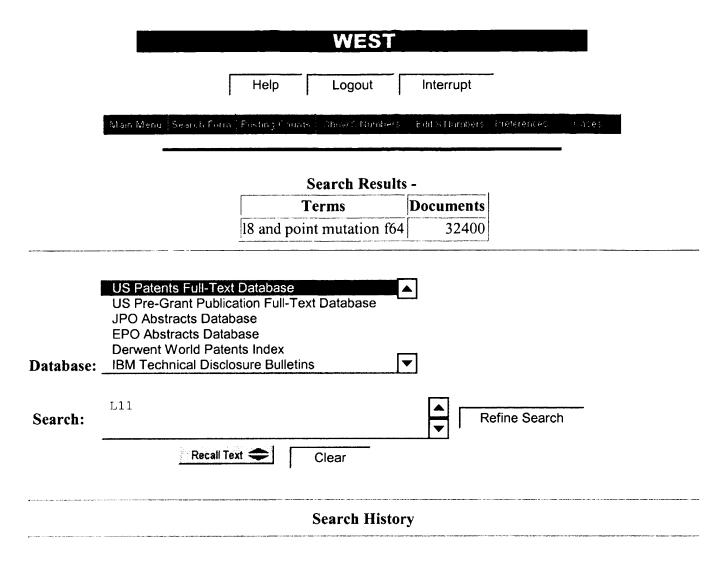
wherein said amino acid substitution that is at position 163 is V163A and said amino acid substitution at position 148 is H148R.

62. The functional fluorescent protein of claim 43,

further comprising an amino acid substitution that is at position 212 or 123.

63. The functional fluorescent protein of claim 62,

wherein said <u>amino acid substitution</u> that is at position 212 is N212K and said <u>amino</u> acid substitution at position 123 is I123V.



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DB=US	DB=USPT; $PLUR=YES$; $OP=OR$						
<u>L11</u>	18 and point mutation f64	32400	<u>L11</u>				
<u>L10</u>	19 and 18	1	<u>L10</u>				
<u>L9</u>	amino acid substitution	720866	<u>L9</u>				
<u>L8</u>	5777079.pn.	1	<u>L8</u>				
<u>L7</u>	16 and 13	2	<u>L7</u>				
<u>L6</u>	encoding DNA and 11	120990	<u>L6</u>				
<u>L5</u>	13 and L4	0	<u>L5</u>				
<u>L4</u>	jones.in.	11873	<u>L4</u>				
<u>L3</u>	11 and L2	83	<u>L3</u>				
<u>L2</u>	stubbs.in.	252	<u>L2</u>				
<u>L1</u>	modified green fluorescent protein	903177	<u>L1</u>				

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Search Results - Record(s) 1 through 10 of 83 returned.

L3: Entry 1 of 83

File: USPT

Aug 5, 2003

US-PAT-NO: 6602539

DOCUMENT-IDENTIFIER: US 6602539 B2

TITLE: Cooked bean product having reduced solids content and improved viscosity

DATE-ISSUED: August 5, 2003

INVENTOR - INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME Stubbs; Timothy A. Gurnee ILBattle; Betsy O. Schaumburg ILMcPherson; Andrew E. Mt. Prospect ILMitchell; Christopher J. Chicago ILSwenson; Bradley J. Grayslake IL

US-CL-CURRENT: 426/634; 426/629

Full - Title | Otation | Front | Review | Clarimistion | Date | Reference | Septience | Attachment: | Claims | 1900 | Orange | Orange |

_ _ 2. Document ID: US 6572822 B2

L3: Entry 2 of 83

File: USPT

Jun 3, 2003

US-PAT-NO: 6572822

DOCUMENT-IDENTIFIER: US 6572822 B2

TITLE: Visual blood glucose test strip

DATE-ISSUED: June 3, 2003

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Jurik; Franklin A.PleasantonCAStubbs; AndreaPalo AltoCADao; Mimi DiemmySan JoseCAChang; CarolSan FranciscoCA

US-CL-CURRENT: 422/56; 422/58, 422/61, 436/170, 436/95

Full Title Utation Front Remem Clarifocation Date Researce Sequence: Attachment, Claims DMC Founders Cinade

☐ 3. Document ID: US 6531322 B1

Record List Display

L3: Entry 3 of 83

File: USPT

Mar 11, 2003

US-PAT-NO: 6531322

DOCUMENT-IDENTIFIER: US 6531322 B1

TITLE: Visual blood glucose test strip

DATE-ISSUED: March 11, 2003

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Jurik; Franklin A.PleasantonCAStubbs; AndreaPalo AltoCADao; Mimi DiemmySan JoseCAChang; CarolSan FranciscoCA

US-CL-CURRENT: 436/95; 422/56, 422/58, 436/170, 436/85

Fell Title Citation Front Review Classification Date Reference Sequences ettachitects Claims Find Chain best Image

L3: Entry 4 of 83

File: USPT Feb 18, 2003

US-PAT-NO: 6522925

DOCUMENT-IDENTIFIER: US 6522925 B1

TITLE: System and method for detection enhancement programming

DATE-ISSUED: February 18, 2003

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Gilkerson; James O. Stillwater MN
Conley; Vickie L. Woodbury MN
Stubbs; Scott Maple Grove MN
Lang; Douglas J. Arden Hills MN

US-CL-CURRENT: 607/30

Full Title | Citation | Front | Review | Hassimilation | Date | Reference | Sequences | Attachments | Claims | Finit | Diagnol Desc. | In the

L3: Entry 5 of 83 File: USPT Dec 10, 2002

US-PAT-NO: 6493579

DOCUMENT-IDENTIFIER: US 6493579 B1

TITLE: System and method for detection enhancement programming

DATE-ISSUED: December 10, 2002

INVENTOR - INFORMATION:

Record List Display

NAME CITY STATE ZIP CODE COUNTRY

Gilkerson; James O. Stillwater MN
Conley; Vickie L. Woodbury MN
Stubbs; Scott Maple Grove MN
Lang; Douglas J. Arden Hills MN

US-CL-CURRENT: 607/5; 607/31

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachment: | Foot | Draw Desc | Incorp-

L3: Entry 6 of 83 File: USPT

SPT Sep 24, 2002

US-PAT-NO: 6455614

DOCUMENT-IDENTIFIER: US 6455614 B1

TITLE: Chlorine-free, zero voc, waterborne adhesion promoter for polyolefinic

substrates

DATE-ISSUED: September 24, 2002

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Jackson; Michael L. LaGrange IL

Stubbs; Frank A. Schererville IN

Mecozzi; Joseph M. Hammond IN

Miklos; David J. Berwyn IL

Neymark; Alexander L. Chicago IL

US-CL-CURRENT: 523/401; 523/406, 523/407, 523/439, 525/117

Full Title Chatton Front Remem Classification Cate Reservoire Sequences Attachined - Foot Gram Cycle Image

L3: Entry 7 of 83 File: USPT Sep 10, 2002

US-PAT-NO: 6447527

DOCUMENT-IDENTIFIER: US 6447527 B1

** See image for Certificate of Correction **

TITLE: Apparatus and methods for the penetration of tissue

DATE-ISSUED: September 10, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Thompson; Ronald J. Ft. Thomas KY 41075 Stubbs; Jack B. Waynesville OH 45068

US-CL-CURRENT: 606/174

L3: Entry 8 of 83

File: USPT

Aug 27, 2002

US-PAT-NO: 6441058

DOCUMENT-IDENTIFIER: US 6441058 B2

TITLE: Abrasive articles having abrasive layer bond system derived from solid, dry-coated binder precursor particles having a fusible, radiation curable component

DATE-ISSUED: August 27, 2002

INVENTOR - INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME Thurber; Ernest L. Woodbury MN Larson; Eric G. Lake Elmo MN St. Paul MN Dahlke; Gregg D. DeVoe; Robert J. Oakdale MN Kirk; Alan R. Cottage Grove MN Meierotto; Mark R. Hudson WI Stubbs; Roy Nuneaton GB

US-CL-CURRENT: <u>522/96</u>; <u>522/103</u>, <u>522/107</u>, <u>522/170</u>, <u>522/173</u>, <u>522/174</u>, <u>522/175</u>, <u>522/179</u>, <u>522/181</u>, <u>522/182</u>

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L3: Entry 9 of 83

File: USPT

Aug 21, 2001

US-PAT-NO: 6277160

DOCUMENT-IDENTIFIER: US 6277160 B1

** See image for Certificate of Correction **

TITLE: Abrasive article and method of making such article

DATE-ISSUED: August 21, 2001

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Stubbs; Roy Nuneaton GB Culler; Scott R. Burnsville MN Liepa; Mara E. St. Paul MN Bange; Donna W. Eagan MN Haas: John D. Roseville MN

US-CL-CURRENT: 51/295; 51/293, 51/298, 51/309

Fell Title Citation Front Review Classification Date Reterence Sequences Attachments - Find Francisco Image

L3: Entry 10 of 83

File: USPT

May 8, 2001

US-PAT-NO: 6228133

DOCUMENT-IDENTIFIER: US 6228133 B1

** See image for Certificate of Correction **

TITLE: Abrasive articles having abrasive layer bond system derived from solid, dry-coated binder precursor particles having a fusible, radiation curable component

DATE-ISSUED: May 8, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Thurber; Ernest L.	Woodbury	MN			
Larson; Eric G.	Lake Elmo	MN			
Dahlke; Gregg D.	St. Paul	MN			
DeVoe; Robert J.	Oakdale	MN			
Kirk; Alan R.	Cottage Grove	MN			
Meierotto; Mark R.	Hudson	WI			
Stubbs; Roy	Nuneaton				GB

US-CL-CURRENT: 51/295; 51/297, 51/298

Title Citation Front Review Classifi	lation : Trate : Reference Sequences withorhiments	Finds - Draw Deeve 1 Tri sepe-
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Previous Page Next Page

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Search Results - Record(s) 61 through 70 of 83 returned.

☐ 61. Document ID: US 5071661 A

L3: Entry 61 of 83

File: USPT

Dec 10, 1991

US-PAT-NO: 5071661

DOCUMENT-IDENTIFIER: US 5071661 A

TITLE: Process for dehydrating potato products

DATE-ISSUED: December 10, 1991

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Stubbs; Clifford A. Iona ID
Willard; Miles J. Idaho Falls ID

US-CL-CURRENT: 426/96; 426/102, 426/272, 426/273, 426/292, 426/293, 426/464, 426/473, 426/637

Foll Title Citation Front Remain Classification Date Reference Dequation. Altochnicit.

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☐ 62. Document ID: US 5052410 A

L3: Entry 62 of 83

File: USPT

Oct 1, 1991

US-PAT-NO: 5052410

DOCUMENT-IDENTIFIER: US 5052410 A

TITLE: Device for controlling eating and smoking habits

DATE-ISSUED: October 1, 1991

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Stubbs; James M. Rockingham NC 28379

US-CL-CURRENT: 128/859; 128/860, 604/909

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L3: Entry 63 of 83 File: USPT Jul 9, 1991

US-PAT-NO: 5029959

DOCUMENT-IDENTIFIER: US 5029959 A

** See image for Certificate of Correction **

Final Laurence of Burster

TITLE: Multiple ring guide for payout testing of optical fibers

DATE-ISSUED: July 9, 1991

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Stubbs; Scott F. Tucson AZ

US-CL-CURRENT: 385/134; 242/125, 242/157R, 242/566, 385/123, 57/352, 57/71

Full Little Editation Front Review Clarimitation Date Reference Sequences Attachamerts

File: USPT Mar 26, 1991

US-PAT-NO: 5003590

L3: Entry 64 of 83

DOCUMENT-IDENTIFIER: US 5003590 A

TITLE: Encoding an optical video disc to inhibit video tape recording

DATE-ISSUED: March 26, 1991

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Lechner; Bernard J. Princeton NJ

Stubbs; Graham S. Poway CA

Leonard; Eugene Sands Point NY

US-CL-CURRENT: 380/204; 360/60, 380/214

Full | Title | Citation | Front | Review | Classification | Cate | Reference | Sequence | Attachitects | 1960 | Craw Desc | Inlage

☐ 65. Document ID: US 4868785 A

L3: Entry 65 of 83 File: USPT Sep 19, 1989

US-PAT-NO: 4868785

DOCUMENT-IDENTIFIER: US 4868785 A

** See image for Certificate of Correction **

TITLE: Block diagram editor system and method for controlling electronic instruments

DATE-ISSUED: September 19, 1989

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Jordan; Dale A. Aloha OR

Fitzsimmons; Lynne A. Portland OR Greenseth; William A. Portland OR Hoffman; Gregory L. Beaverton OR Stubbs; David D. Portland OR

US-CL-CURRENT: 345/440

Full | Title | Chango | Front | Review | Classification | Crate | Reference | Scriptificate | Attachment | Finit | Change Cess | Inside

☐ 66. Document ID: US 4812996 A

L3: Entry 66 of 83

File: USPT

Mar 14, 1989

US-PAT-NO: 4812996

DOCUMENT-IDENTIFIER: US 4812996 A

TITLE: Signal viewing instrumentation control system

DATE-ISSUED: March 14, 1989

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

<u>Stubbs</u>; David D. Portland OR

US-CL-CURRENT: 702/123; 324/121R, 324/76.19, 324/76.24, 345/440, 345/440.1, 345/661,

345/808, 345/970

Full Dite Citation Front Review Classification Date Reference Sciences, Attachment. Find Control (1990) (1990)

☐ 67. Document ID: US 4760797 A

L3: Entry 67 of 83 File: USPT Aug 2, 1988

US-PAT-NO: 4760797

DOCUMENT-IDENTIFIER: US 4760797 A

TITLE: Method and apparatus for automated tie detection and tamping

DATE-ISSUED: August 2, 1988

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Stubbs; John L. Charlotte NC
Patton; Wesley H. Atlanta GA
Thompson; Jeffrey L. Lawrenceville GA

US-CL-CURRENT: 104/12; 180/168, 246/187B, 701/19, 701/50

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☐ 68. Document ID: US 4597500 A

L3: Entry 68 of 83 File: USPT Jul 1, 1986

US-PAT-NO: 4597500

DOCUMENT-IDENTIFIER: US 4597500 A

TITLE: Tamper-resistant closures for containers

DATE-ISSUED: July 1, 1986

INVENTOR - INFORMATION:

NAME

CITY

STATE

ZIP CODE

COUNTRY

Stubbs; Peter

Dartford

Full Title Citation: Front Review Classification Cate Reference Sequence: Attachment:

GB

US-CL-CURRENT: 215/256; 215/258

Finds - Brain Bess - In age

L3: Entry 69 of 83

File: USPT

Apr 15, 1986

US-PAT-NO: 4582680

DOCUMENT-IDENTIFIER: US 4582680 A

TITLE: Multiphase backing materials for piezoelectric broadband transducers

DATE-ISSUED: April 15, 1986

INVENTOR - INFORMATION:

NAME

CITY

STATE

ZIP CODE

Bar-Cohen; Yoseph

Dayton

COUNTRY

Stubbs; David A.

Waynesville

OH OH

Hoppe; Wally C.

Huber Heights

OH

US-CL-CURRENT: 419/23; 29/25.35, 419/<u>31, 419/32, 419/48, 419/5, 419/60, 419/8</u>

Full Title Citation: Front Review Clariforation: Date Reference Sequence: Attachmist:

Party : Draw Costo : Irospe

☐ 70. Document ID: US 4581070 A

L3: Entry 70 of 83

File: USPT

Apr 8, 1986

US-PAT-NO: 4581070

DOCUMENT-IDENTIFIER: US 4581070 A

TITLE: Multiphase backing materials for piezoelectric broadband transducers

DATE-ISSUED: April 8, 1986

INVENTOR - INFORMATION:

NAME

CITY

STATE

COUNTRY

ZIP CODE

Bar-Cohen; Yoseph

Dayton

OH

Stubbs; David A. Hoppe; Wally C.

Waynesville Huber Heights OH OH

US-CL-CURRENT: 75/247; 419/23, 419/5, 419/8, 420/555, 420/563, 420/589, 428/546, <u>428/570</u>, <u>428/929</u>, <u>75/228</u>, <u>75/245</u>

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<u>Previous Page</u> <u>Next Page</u>